Amendments to the Specification

Please replace the paragraph spanning pages 4 and 5 with the following paragraph:

Figure 10 shows the results of the WIQ severity of claudication for the three patient groups in the phase II clinical study at day 90 (FIG. 10A) and day 180 (FIG. 10B). Values represent the percentage of patients in each group indicating an improvement, no change, or worsening of this condition.

Please replace the paragraph at page 5, lines 3-7, with the following paragraph:

Figure 11 shows the severity scores at baseline, day 90, and day 180 for distance, speed, and stair climbing for each group. The figure demonstrates that the results for the single–dose group were better than the results for the placebo group for WIQ distance (FIG. 11A), speed (FIG. 11B), and stair climbing (FIG. 11C). The figure is shown with a scale where higher scores are better.

Please replace the paragraph at page 5, lines 13-18, with the following paragraph:

Figure 14 shows the measured ABI (ankle-brachial index) (FIG. 14A) for the three patient groups of the phase II clinical study, when subjects having an ABI > 1.2 at anytime (i.e., baseline, day 90, and/or day 180) are excluded from the analysis. A baseline measurement, a day-90 measurement, and the corresponding change between the baseline and day-90 measurement are indicated. The mean change in ABI (FIG. 14B) is also shown for the three patient groups.

Please replace the paragraph spanning pages 17-18 with the following paragraph:

Thus, the determination of percent identity between any two sequences can be accomplished using a mathematical algorithm. One preferred, non-limiting example of a

mathematical algorithm utilized for the comparison of sequences is the algorithm of Myers and Miller (1988) *CABIOS 4*:11-17. Such an algorithm is utilized in the ALIGN program (version 2.0), which is part of the GCG sequence alignment software package. A PAM120 weight residue table, a gap length penalty of 12, and a gap penalty of 4 can be used with the ALIGN program when comparing amino acid sequences. Another preferred, nonlimiting example of a mathematical algorithm for use in comparing two sequences is the algorithm of Karlin and Altschul (1990) *Proc. Natl. Acad. Sci. USA 87*:2264, modified as in Karlin and Altschul (1993) *Proc. Natl. Acad. Sci. USA 90*:5873-5877. Such an algorithm is incorporated into the NBLAST and XBLAST programs of Altschul *et al.* (1990) *J. Mol. Biol. 215*:403. BLAST nucleotide searches can be performed with the NBLAST program, score = 100, wordlength = 12, to obtain nucleotide sequences homologous to a nucleotide sequence encoding the polypeptide of interest. BLAST protein searches can be performed with the XBLAST program, score = 50, wordlength = 3, to obtain amino acid sequences homologous to the polypeptide of interest. To obtain gapped alignments for comparison purposes, Gapped BLAST can be utilized as described in Altschul *et al.* (1997) *Nucleic Acids Res. 25*:3389. Alternatively, PSI-Blast can be used to perform an iterated search that detects distant relationships between molecules. See Altschul *et al.* (1997) *supra*. When utilizing BLAST, Gapped BLAST, and PSI-Blast programs, the default parameters of the respective programs (e.g., XBLAST and NBLAST) can be used. *See* ~~www.ncbi.nlm.nih.gov~~ ncbi.nlm.nih.gov (a www prefix must be used). Also see the ALIGN program (Dayhoff (1978) in *Atlas of Protein Sequence and Structure* 5:Suppl. 3 (National Biomedical Research Foundation, Washington, D.C.) and programs in the Wisconsin Sequence Analysis Package, Version 8 (available from Genetics Computer Group, Madison, Wisconsin), for example, the GAP program, where default parameters of the programs are utilized.